



~~14~~ 6

SEQUENCE LISTING

~~TRADEMA~~ Junghans, Richard P.

<120> Chimeric Effector Cell Receptors Against Carcinoembryonic Antigen
<130> 002
<140> 10/006,771
<141> 2001-12-10
<150> 60/250,090
<151> 2000-11-30
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<170> PatentIn version 3.1
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<221> CDS
<222> (2428)..(3759)
<223> Chimeric IgTCR sequence contained in retroviral vector. Retroviral vector sequence (non-coding regions) are incidental to the invention. The translated (coding region) is relevant to the invention. (pertinent to Figure 3.)

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Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr			
235	240	245	
tgg ggc caa ggg acc ccg gtc acc gtc tcc agt gct aag ccc acc acg			3222
Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser Ala Lys Pro Thr Thr			
250	255	260	265
acg cca gcg ccg cga cca aca ccg gcg ccc acc atc gcg tcg cag			3270
Thr Pro Ala Pro Arg Pro Pro Thr Pro Ala Pro Thr Ile Ala Ser Gln			
270	275	280	
ccc ctg tcc ctg cgc cca gag gcg gct cgg cca gcg gcg ggg ggc gca			3318
Pro Leu Ser Leu Arg Pro Glu Ala Ala Arg Pro Ala Ala Gly Gly Ala			
285	290	295	
gtg cac acg agg ggg ctg gac ttc gcc ctg gat ccc aaa ctc tgc tac			3366
Val His Thr Arg Gly Leu Asp Phe Ala Leu Asp Pro Lys Leu Cys Tyr			
300	305	310	
ctg ctg gat gga atc ctc ttc atc tat ggt gtc att ctc act gcc ttg			3414
Leu Leu Asp Gly Ile Leu Phe Ile Tyr Gly Val Ile Leu Thr Ala Leu			
315	320	325	
ttc ctg aga gtg aag ttc agc agg agc gca gag ccc ccc gcg tac cag			3462
Phe Leu Arg Val Lys Phe Ser Arg Ser Ala Glu Pro Pro Ala Tyr Gln			
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cag ggc cag aac cag ctc tat aac gag ctc aat cta gga cga aga gag			3510
Gln Gly Gln Asn Gln Leu Tyr Asn Glu Leu Asn Leu Gly Arg Arg Glu			
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gag tac gat gtt ttg gac aag aga cgt ggc cgg gac cct gag atg ggg			3558
Glu Tyr Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly			
365	370	375	
gga aag ccg aga agg aag aac cct cag gaa ggc ctg tac aat gaa ctg			3606
Gly Lys Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu			
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cag aaa gat aag atg gcg gag gcc tac agt gag att ggg atg aaa ggc			3654
Gln Lys Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly			
395	400	405	
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Glu Arg Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser			
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aca gcc acc aag gac acc tac gac gcc ctt cac atg cag gcc ctg ccc			3750
Thr Ala Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro			
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Pro Arg			

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<212> PRT
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Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala
20 25 30

Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val
35 40 45

Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
50 55 60

Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly Val Pro Ser Arg
65 70 75 80

Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser
85 90 95

Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Ser Leu
100 105 110

Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly
115 120 125

Ser Gly Ser Gly Gly Ser Gly Ser Gly Gly Ser Gly Ser Glu Val Gln
130 135 140

Leu Val Glu Ser Gly Gly Val Val Gln Pro Gly Arg Ser Leu Arg
145 150 155 160

Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe Thr Thr Tyr Trp Met Ser
165 170 175

Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile Gly Glu Ile
180 185 190

His Pro Asp Ser Ser Thr Ile Asn Tyr Ala Pro Ser Leu Lys Asp Arg
195 200 205

Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Phe Leu Gln Met
210 215 220

Asp Ser Leu Arg Pro Glu Asp Thr Gly Val Tyr Phe Cys Ala Ser Leu
225 230 235 240

Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp Gly Gln Gly Thr Pro Val
245 250 255

Thr Val Ser Ser Ala Lys Pro Thr Thr Pro Ala Pro Arg Pro Pro
260 265 270

Thr Pro Ala Pro Thr Ile Ala Ser Gln Pro Leu Ser Leu Arg Pro Glu
275 280 285

Ala Ala Arg Pro Ala Ala Gly Gly Ala Val His Thr Arg Gly Leu Asp
290 295 300

Phe Ala Leu Asp Pro Lys Leu Cys Tyr Leu Leu Asp Gly Ile Leu Phe
305 310 315 320

Ile Tyr Gly Val Ile Leu Thr Ala Leu Phe Leu Arg Val Lys Phe Ser
325 330 335

Arg Ser Ala Glu Pro Pro Ala Tyr Gln Gln Gly Gln Asn Gln Leu Tyr
340 345 350

Asn Glu Leu Asn Leu Gly Arg Arg Glu Glu Tyr Asp Val Leu Asp Lys

355

360

365

Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys Pro Arg Arg Lys Asn
370 375 380

Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys Asp Lys Met Ala Glu
385 390 395 400

Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg Arg Arg Gly Lys Gly
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His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala Thr Lys Asp Thr Tyr
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Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
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<210> 3

<211> 422

<212> DNA

<213> Homo sapiens and Mus sp.

<220>

<221> CDS

<222> (8)..(421)

<223> hMn14 VH, humanized (CDR-grafted) anti-CEA antibody heavy chain V
region (aa20-138) with leader (aal-19) (pertinent to Fig. 4A.)

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aca ggt gtc cac tcc gag gtc caa ctg gtg gag agc ggt gga ggt gtt 97
Thr Gly Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Val
15 20 25 30

gtg caa cct ggc cgg tcc ctg cgc ctg tcc tgc tcc gca tct ggc ttc 145
Val Gln Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe
35 40 45

gat ttc acc aca tat tgg atg agt tgg gtg aga cag gca cct gga aaa 193
Asp Phe Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys
50 55 60

ggt ctt gag tgg att gga gaa att cat cca gat agc agt acg att aac 241
Gly Leu Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn
65 70 75

tat gcg ccg tct cta aag gat aga ttt aca ata tcg cga gac aac gcc 289

Tyr Ala Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala
80 85 90
aag aac aca ttg ttc ctg caa atg gac agc ctg aga ccc gaa gac acc 337
Lys Asn Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr
95 100 105 110
ggg gtc tat ttt tgt gca agc ctt tac ttc ggc ttc ccc tgg ttt gct 385
Gly Val Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala
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Tyr Trp Gly Gln Gly Thr Pro Val Thr Val Ser Ser
130 135

<210> 4
<211> 138
<212> PRT
<213> Homo sapiens and Mus sp.

<400> 4

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Val His Ser Glu Val Gln Leu Val Glu Ser Gly Gly Val Val Gln
20 25 30

Pro Gly Arg Ser Leu Arg Leu Ser Cys Ser Ala Ser Gly Phe Asp Phe
35 40 45

Thr Thr Tyr Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
50 55 60

Glu Trp Ile Gly Glu Ile His Pro Asp Ser Ser Thr Ile Asn Tyr Ala
65 70 75 80

Pro Ser Leu Lys Asp Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn
85 90 95

Thr Leu Phe Leu Gln Met Asp Ser Leu Arg Pro Glu Asp Thr Gly Val
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Tyr Phe Cys Ala Ser Leu Tyr Phe Gly Phe Pro Trp Phe Ala Tyr Trp
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Gly Gln Gly Thr Pro Val Thr Val Ser Ser
130 135

<210> 5
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 <212> DNA
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 <220>
 <221> CDS
 <222> (14)..(712)
 <223> hMN14 VLCK, humanized (CDR-grafted) anti-CEA antibody kappa light chain V region (aa20-126), with human constant CK domain (aa127-232) and leader (aa1-19). (pertinent to Figure 4B.)

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 Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala
 1 5 10

 aca gct aca ggt gtc cac tcc gac atc cag ctg acc cag agc cca agc 97
 Thr Ala Thr Gly Val His Ser Asp Ile Gln Leu Thr Gln Ser Pro Ser
 15 20 25

 agc ctg agc gcc agc gtg ggt gac aga gtg acc atc acc tgt aag gcc 145
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala
 30 35 40

 agt cag gat gtg ggt act tct gta gct tgg tac cag cag aag cca ggt 193
 Ser Gln Asp Val Gly Thr Ser Val Ala Trp Tyr Gln Gln Lys Pro Gly
 45 50 55 60

 aag gct cca aag ctg ctg atc tac tgg aca tcc acc cgg cac act ggt 241
 Lys Ala Pro Lys Leu Leu Ile Tyr Trp Thr Ser Thr Arg His Thr Gly
 65 70 75

 gtg cca agc aga ttc agc ggt agc ggt acc gac ttc acc ttc 289
 Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe
 80 85 90

 acc atc agc agc ctc cag cca gag gac atc gcc acc tac tac tgc cag 337
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln
 95 100 105

 caa tat agc ctc tat cgg tcg ttc ggc caa ggg acc aag gtg gaa atc 385
 Gln Tyr Ser Leu Tyr Arg Ser Phe Gly Gln Gly Thr Lys Val Glu Ile
 110 115 120

 aaa cga act gtg gct gca cca tct gtc ttc atc ttc cgg cca tct gat 433
 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
 125 130 135 140

 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac 481
 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
 145 150 155

 ttc tat ccc aga gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc 529

Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys
130 135 140

Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg
145 150 155 160

Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn
165 170 175

Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser
180 185 190

Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys
195 200 205

Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr
210 215 220

Lys Ser Phe Asn Arg Gly Glu Cys
225 230